



Revised Sequence Listing filed 2006-07-26
SEQUENCE LISTING

<110> KATO, Seishi
NAGATA, Naoki
FUJIMURA, Naoko
KOBAYASHI, Midori
ITO, Koichi
ISHIZUKA, Yoshiko

<120> A Method For Producing An Antibody By Gene Immunization

<130> 2002_0400A

<140> 10/088,859
<141> 2002-05-29

<150> PCT/JP01/06371
<151> 2001-07-24

<150> PCT2000-222743
<151> 2000-07-24

<150> JP2000-254407
<151> 2000-08-24

<160> 18

<170> PatentIn version 3.3

<210> 1
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<212> DNA
<213> Homo sapiens

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<222> (151)..(600)

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aatcaaaacg ctgattaaaaa gaagcacggat atg atg acc aaa cat aaa aag tgt 174
Met Met Thr Lys His Lys Lys Cys
1 5

ttt ata att gtt gtt tta ata aca act aat att att act ctg ata 222
Phe Ile Ile Val Gly Val Leu Ile Thr Thr Asn Ile Ile Thr Leu Ile
10 15 20

gtt aaa cta act cga gat tct cag agt tta tgc ccc tat gat tgg att 270
Val Lys Leu Thr Arg Asp Ser Gln Ser Leu Cys Pro Tyr Asp Trp Ile
25 30 35 40

ggt ttc caa aac aaa tgc tat tat ttc tct aaa gaa gaa gga gat tgg 318
Gly Phe Gln Asn Lys Cys Tyr Tyr Phe Ser Lys Glu Glu Gly Asp Trp
45 50 55

aat tca agt aaa tac aac tgt tcc actcaa cat gcc gac cta act ata 366
Asn Ser Ser Lys Tyr Asn Cys Ser Thr Gln His Ala Asp Leu Thr Ile
60 65 70

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att gac aac ata gaa gaa atg aat ttt ctt agg cg ^g tat aaa tgc agt Ile Asp Asn Ile Glu Glu Met Asn Phe Leu Arg Arg Tyr Lys Cys Ser 75 80 85	414
tct gat cac tgg att gga ctg aag atg gca aaa aat cga aca gga caa Ser Asp His Trp Ile Gly Leu Lys Met Ala Lys Asn Arg Thr Gly Gln 90 95 100	462
tgg gta gat gga gct aca ttt acc aaa tcg ttt ggc atg aga ggg agt Trp Val Asp Gly Ala Thr Phe Thr Lys Ser Phe Gly Met Arg Gly Ser 105 110 115 120	510
gaa gga tgt gcc tac ctc agc gat gat ggt gca gca aca gct aga tgt Glu Gly Cys Ala Tyr Leu Ser Asp Asp Gly Ala Ala Thr Ala Arg Cys 125 130 135	558
tac acc gaa aga aaa tgg att tgc agg aaa aga ata cac taa Tyr Thr Glu Arg Lys Trp Ile Cys Arg Lys Arg Ile His 140 145	600
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<212> PRT
<213> Homo sapiens

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Ser Leu Cys Pro Tyr Asp Trp Ile Gly Phe Gln Asn Lys Cys Tyr Tyr 35 40 45
Phe Ser Lys Glu Glu Gly Asp Trp Asn Ser Ser Lys Tyr Asn Cys Ser 50 55 60
Thr Gln His Ala Asp Leu Thr Ile Ile Asp Asn Ile Glu Glu Met Asn 65 70 75 80
Phe Leu Arg Arg Tyr Lys Cys Ser Ser Asp His Trp Ile Gly Leu Lys 85 90 95
Met Ala Lys Asn Arg Thr Gly Gln Trp Val Asp Gly Ala Thr Phe Thr 100 105 110
Lys Ser Phe Gly Met Arg Gly Ser Glu Gly Cys Ala Tyr Leu Ser Asp 115 120 125

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Asp Gly Ala Ala Thr Ala Arg Cys Tyr Thr Glu Arg Lys Trp Ile Cys
130 135 140

Arg Lys Arg Ile His
145

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<212> DNA
<213> *Homo sapiens*

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<222> (30)..(503)

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10			15						20							

agt gac gtg ctg cag cgg gac ttg cga aag gtg ctg gac cat cga gac 149
 Ser Asp Val Leu Gln Arg Asp Leu Arg Lys Val Leu Asp His Arg Asp
 25 30 35 40

aag gta tat gag cag ctg gcc aaa tac ctt caa ctg aga aat gtc att
Lys Val Tyr Glu Gln Leu Ala Lys Tyr Leu Gln Leu Arg Asn Val Ile
45 50 55 197

gag cga ctc cag gaa gct aag cac tcg gag tta tat atg cag gtg gat 245
 Glu Arg Leu Gln Glu Ala Lys His Ser Glu Leu Tyr Met Gln Val Asp
 60 65 70

ttg ggc tgt aac ttc ttc gtt gac aca gtg gtc cca gat act tca cgc
 Leu Gly Cys Asn Phe Phe Val Asp Thr Val Val Pro Asp Thr Ser Arg
 75 80 85 293

atc tat gtg gcc ctg gga tat ggt ttt ttc ctg gag ttg aca ctg gca 341
 Ile Tyr Val Ala Leu Gly Tyr Gly Phe Phe Leu Glu Leu Thr Leu Ala
 90 95 100

gaa gct ctc aag ttc att gat cgt aag agc tct ctc ctc aca gag ctc 389
 Glu Ala Leu Lys Phe Ile Asp Arg Lys Ser Ser Leu Leu Thr Glu Leu
 105 110 115 120

agc aac agc ctc acc aag gac tcc atg aat atc aaa gcc cat atc cac
 Ser Asn Ser Leu Thr Lys Asp Ser Met Asn Ile Lys Ala His Ile His
 125 130 135 437

atg ttg cta gag ggg ctt aga gaa cta caa ggc ctg cag aat ttc cca 485
 Met Leu Leu Glu Gly Leu Arg Glu Leu Gln Gly Leu Gln Asn Phe Pro
 140 145 150

gag aag cct cac cat tga cttttcccccc ccatccttag acattaaaga 533
Glu Lys Pro His His

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155

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548

<210> 4
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<212> PRT
<213> Homo sapiens

<400> 4

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Arg Lys Val Leu Asp His Arg Asp Lys Val Tyr Glu Gln Leu Ala Lys
35 40 45

Tyr Leu Gln Leu Arg Asn Val Ile Glu Arg Leu Gln Glu Ala Lys His
50 55 60

Ser Glu Leu Tyr Met Gln Val Asp Leu Gly Cys Asn Phe Phe Val Asp
65 70 75 80

Thr Val Val Pro Asp Thr Ser Arg Ile Tyr Val Ala Leu Gly Tyr Gly
85 90 95

Phe Phe Leu Glu Leu Thr Leu Ala Glu Ala Leu Lys Phe Ile Asp Arg
100 105 110

Lys Ser Ser Leu Leu Thr Glu Leu Ser Asn Ser Leu Thr Lys Asp Ser
115 120 125

Met Asn Ile Lys Ala His Ile His Met Leu Leu Glu Gly Leu Arg Glu
130 135 140

Leu Gln Gly Leu Gln Asn Phe Pro Glu Lys Pro His His
145 150 155

<210> 5
<211> 30
<212> DNA
<213> Artificial

<220>
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<220>
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<400> 6
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<212> DNA
<213> Homo sapiens

<220>
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<222> (25)..(915)

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Gln Gln Leu Gly Leu Leu Gly Cys Leu Gly His Gly Ala Leu Val Leu
10 15 20 25

caa ctc ctc tcc ttc atg ctc ttg gct ggg gtc ctg gtg gcc atc ctt 147
Gln Leu Leu Ser Phe Met Leu Leu Ala Gly Val Leu Val Ala Ile Leu
30 35 40

gtc caa gtg tcc aag gtc ccc agc tcc cta agt cag gaa caa tcc gag 195
Val Gln Val Ser Lys Val Pro Ser Ser Leu Ser Gln Glu Gln Ser Glu
45 50 55

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caa gac gca atc tac cag aac ctg acc cag ctt aaa gct gca gtg ggt Gln Asp Ala Ile Tyr Gln Asn Leu Thr Gln Leu Lys Ala Ala Val Gly 60 65 70	243
gag ctc tca gag aaa tcc aag ctg cag gag atc tac cag gag ctg acc Glu Leu Ser Glu Lys Ser Lys Leu Gln Glu Ile Tyr Gln Glu Leu Thr 75 80 85	291
cag ctg aag gct gca gtg ggt gag ttg cca gag aaa tcc aag ctg cag Gln Leu Lys Ala Ala Val Gly Glu Leu Pro Glu Lys Ser Lys Leu Gln 90 95 100 105	339
gag atc tac cag gag ctg acc cgg ctg aag gct gca gtg ggt gag ttg Glu Ile Tyr Gln Glu Leu Thr Arg Leu Lys Ala Ala Val Gly Glu Leu 110 115 120	387
cca gag aaa tcc aag ctg cag gag atc tac cag gag ctg acc cgg ctg Pro Glu Lys Ser Lys Leu Gln Glu Ile Tyr Gln Glu Leu Thr Arg Leu 125 130 135	435
aag gct gca gtg ggt gag ttg cca gag aaa tcc aag ctg cag gag atc Lys Ala Ala Val Gly Glu Leu Pro Glu Lys Ser Lys Leu Gln Glu Ile 140 145 150	483
tac cag gag ctg acc cgg ctg aag gct gca gtg ggt gag ttg cca gag Tyr Gln Glu Leu Thr Arg Leu Lys Ala Ala Val Gly Glu Leu Pro Glu 155 160 165	531
aaa tcc aag ctg cag gag atc tac cag gag ctg acg gag ctg aag gct Lys Ser Lys Leu Gln Glu Ile Tyr Gln Glu Leu Thr Glu Leu Lys Ala 170 175 180 185	579
gca gtg ggt gag ttg cca gag aaa tcc aag ctg cag gag atc tac cag Ala Val Gly Glu Leu Pro Glu Lys Ser Lys Leu Gln Glu Ile Tyr Gln 190 195 200	627
gag ctg acc cag ctg aag gct gca gtg ggt gag ttg cca gac cag tcc Glu Leu Thr Gln Leu Lys Ala Ala Val Gly Glu Leu Pro Asp Gln Ser 205 210 215	675
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gaa cgc ctg tgc cgc cac tgt ccc aag gac tgg aca ttc ttc caa gga Glu Arg Leu Cys Arg His Cys Pro Lys Asp Trp Thr Phe Phe Gln Gly 235 240 245	771
aac tgt tac ttc atg tct aac tcc cag cgg aac tgg cac gac tcc gtc Asn Cys Tyr Phe Met Ser Asn Ser Gln Arg Asn Trp His Asp Ser Val 250 255 260 265	819
acc gcc tgc cag gaa gtg agg gcc cag ctc gtc gta atc aaa act gct Thr Ala Cys Gln Glu Val Arg Ala Gln Leu Val Val Ile Lys Thr Ala 270 275 280	867
gag gag cag ctt cca gcg gta ctg gaa cag tgg aga acc caa caa tag Glu Glu Gln Leu Pro Ala Val Leu Glu Gln Trp Arg Thr Gln Gln 285 290 295	915
cgggaatgaa gactgtgcgg aatttagtgg cagtggctgg aacgacaatc gatgtgacgt	975

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ctgctagcct cagcctccat tgtggtag cagaacttca cccacttgta agccagcgct	1095
tcttcctcc atccttggac cttcacaaat gccctgagac gttctctgt tcgattttc	1155
atcccctatg aacctgggtc ttattctgtc cttctgatgc ctccaagttt ccctggtgta	1215
gagcttgtgt tcttggccca tccttggagc ttataagtg acctgagtgg gatgcattta	1275
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ccagagaggg catggaggct ccatacaacc tcttccaccc ccacatctt cttgtccta	1575
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<222> (118)..(1236)

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atg aag tat ctc cgg cac cgg cgg ccc aat gcc acc ctc att ctg gcc Met Lys Tyr Leu Arg His Arg Arg Pro Asn Ala Thr Leu Ile Leu Ala	165
1 5 10 15	
atc ggc gct ttc acc ctc ctc ttc agt ctg cta gtg tca cca ccc Ile Gly Ala Phe Thr Leu Leu Leu Phe Ser Leu Leu Val Ser Pro Pro	213
20 25 30	
acc tgc aag gtc cag gag cag cca ccg gcg atc ccc gag gcc ctg gcc Thr Cys Lys Val Gln Glu Gln Pro Pro Ala Ile Pro Glu Ala Leu Ala	261
35 40 45	
tgg ccc act cca ccc acc cgc cca gcc ccg gcc ccg tgc cat gcc aac Trp Pro Thr Pro Pro Thr Arg Pro Ala Pro Ala Pro Cys His Ala Asn	309
50 55 60	
acc tct atg gtc acc cac ccg gac ttc gcc acg cag ccg cag cac gtt Thr Ser Met Val Thr His Pro Asp Phe Ala Thr Gln Pro Gln His Val	357
65 70 75 80	
cag aac ttc ctc ctg tac aga cac tgc cgc cac ttt ccc ctg ctg cag Gln Asn Phe Leu Leu Tyr Arg His Cys Arg His Phe Pro Leu Leu Gln	405
85 90 95	

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atc aag tcc tcc cct agc aac tat gtg cgc cgc gag ctg ctg cgg cgc Ile Lys Ser Ser Pro Ser Asn Tyr Val Arg Arg Glu Leu Leu Arg Arg 115 120 125	501
acg tgg ggc cgc gag cgc aag gta cgg ggt ttg cag ctg cgc ctc ctc Thr Trp Gly Arg Glu Arg Lys Val Arg Gly Leu Gln Leu Arg Leu Leu 130 135 140	549
ttc ctg gtg ggc aca gcc tcc aac ccg cac gag gcc cgc aag gtc aac Phe Leu Val Gly Thr Ala Ser Asn Pro His Glu Ala Arg Lys Val Asn 145 150 155 160	597
cgg ctg ctg gag ctg gag gca cag act cac gga gac atc ctg cag tgg Arg Leu Leu Glu Leu Glu Ala Gln Thr His Gly Asp Ile Leu Gln Trp 165 170 175	645
gac ttc cac gac tcc ttc aac ctc acg ctc aag cag gtc ctg ttc Asp Phe His Asp Ser Phe Asn Leu Thr Leu Lys Gln Val Leu Phe 180 185 190	693
tta cag tgg cag gag aca agg tgc gcc aac gcc agc ttc gtg ctc aac Leu Gln Trp Gln Glu Thr Arg Cys Ala Asn Ala Ser Phe Val Leu Asn 195 200 205	741
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cag gac cat gac cct ggc cgc cac ctc ttc gtg ggg caa ctg atc caa Gln Asp His Asp Pro Gly Arg His Leu Phe Val Gly Gln Leu Ile Gln 225 230 235 240	837
aac gtg ggc ccc atc cgg gct ttt tgg agc aag tac tat gtg cca gag Asn Val Gly Pro Ile Arg Ala Phe Trp Ser Lys Tyr Tyr Val Pro Glu 245 250 255	885
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gag ctt gag gga ctg aag cct gcc tcc cac agc ggc atc cgc acg tct Glu Leu Glu Gly Leu Lys Pro Ala Ser His Ser Gly Ile Arg Thr Ser 305 310 315 320	1077
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tac cga gac ctg ctg gtg cac cgc ttc cta cct tat gag atg ctg Tyr Arg Asp Leu Leu Leu Val His Arg Phe Leu Pro Tyr Glu Met Leu	1173

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340

345

350

ctc atg tgg gat gcg ctg aac cag ccc aac ctc acc tgc ggc aat cag Leu Met Trp Asp Ala Leu Asn Gln Pro Asn Leu Thr Cys Gly Asn Gln 355	360	365	1221
aca cag atc tac tga gtcagcatca gggccccag cctctggcct cctgtttcca Thr Gln Ile Tyr 370			1276
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agtgccaggg aaggtttgag gtttgatgag tgaatattct ggctggcgaa ctcctacaca			1396
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actgtggatg catccgtccc gtttgagtca aagtcttact tccctgctct cacctactca			1576
cagacgggat gctaaggcgt gcacctgcag tggtttaatg gcagataagc tccgtctgca			1636
gttccaggcc agccagaaac tcctgtgtcc acatagagct gacgtgagaa atatcttca			1696
gcccaggaga gagggtcct gatcttaacc ctttcctggg tctcagacaa ctcagaaggt			1756
tgggggata ccagagaggt ggtggaatag gaccgcccc tccttacttg tggatcaaa			1816
tgctgtaatg gtggaggtgt gggcagagga gggaggcaag tgtccttga aagttgttag			1876
agctcagagt ttctgggtc ctcattagga gccccatcc ctgtttccca caagaattca			1936
gagaacagca ctggggctgg aatgatctt aatgggccc aggccaacag gcatatgcct			1996
cactactgcc tggagaagg agagattcag gtcctccagc agcctccctc acccagtag			2056
ttttacagat tacggggggc ccgggtgagc cagtgacccc ctgcagcccc cagcttcagg			2116
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<213> Homo sapiens

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<222> (145)..(693)

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ctt ctg ggg gcc ctg gga acc gcc tgg gct cgg agg agc cag gat	219

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Leu	Leu	Gly	Ala	Leu	Leu	Gly	Thr	Ala	Trp	Ala	Arg	Arg	Ser	Gln	Asp		
10					15				20					25			
ctc	cac	tgt	gga	gca	tgc	agg	gct	ctg	gtg	gat	gaa	cta	gaa	tgg	gaa	267	
Leu	His	Cys	Gly	Ala	Cys	Arg	Ala	Leu	Val	Asp	Glu	Leu	Glu	Trp	Glu		
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Ile	Ala	Gln	Val	Asp	Pro	Lys	Lys	Thr	Ile	Gln	Met	Gly	Ser	Phe	Arg		
									45					55			
atc	aat	cca	gat	ggc	agc	cag	tca	gtg	gtg	gag	gtg	cct	tat	gcc	cgc	363	
Ile	Asn	Pro	Asp	Gly	Ser	Gln	Ser	Val	Val	Glu	Val	Pro	Tyr	Ala	Arg		
									60					70			
tca	gag	gcc	cac	ctc	aca	gag	ctg	ctg	gag	gag	ata	tgt	gac	cgg	atg	411	
Ser	Glu	Ala	His	Leu	Thr	Glu	Leu	Leu	Glu	Glu	Ile	Cys	Asp	Arg	Met		
									75					85			
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Lys	Glu	Tyr	Gly	Glu	Gln	Ile	Asp	Pro	Ser	Thr	His	Arg	Lys	Asn	Tyr		
									90					105			
gta	cgt	gta	gtg	ggc	cgg	aat	gga	gaa	tcc	agt	gaa	ctg	gac	cta	caa	507	
Val	Arg	Val	Val	Gly	Arg	Asn	Gly	Glu	Ser	Ser	Glu	Leu	Asp	Leu	Gln		
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ggc	atc	cga	atc	gac	tca	gat	att	agc	ggc	acc	ctc	aag	ttt	gcg	tgt	555	
Gly	Ile	Arg	Ile	Asp	Ser	Asp	Ile	Ser	Gly	Thr	Leu	Lys	Phe	Ala	Cys		
									125					135			
gag	agc	att	gtg	gag	gaa	tac	gag	gat	gaa	ctc	att	gaa	ttc	ttt	tcc	603	
Glu	Ser	Ile	Val	Glu	Glu	Tyr	Glu	Asp	Glu	Leu	Ile	Glu	Phe	Phe	Ser		
									140					150			
cga	gag	gct	gac	aat	gtt	aaa	gac	aaa	ctt	tgc	agt	aag	cga	aca	gat	651	
Arg	Glu	Ala	Asp	Asn	Val	Lys	Asp	Lys	Leu	Cys	Ser	Lys	Arg	Thr	Asp		
									155					165			
ctt	tgt	gac	cat	gcc	ctg	cac	ata	tgc	cat	gat	gag	cta	tga			693	
Leu	Cys	Asp	His	Ala	Leu	His	Ile	Ser	His	Asp	Glu	Leu					
									170					180			
accactggag	cagcccacac	tggcttgatg	gatcacccccc	aggaggggaa	aatggtgcca											753	
atgcctttta	tatattatgt	ttttactgaa	attaactgaa	aaaatatgaa	accaaaagta											813	
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<210> 12
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<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (73)..(564)

<400> 12
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1 5 10	
gcg gtg ggc gtg ggc gtc gcc gag ctc acg gaa gcc cag cgc cgg ggc Ala Val Gly Val Gly Val Ala Glu Leu Thr Glu Ala Gln Arg Arg Gly	159
15 20 25	
ctg cag gtg gcc ctg gag gaa ttt cac aag cac ccg ccc gtg cag tgg Leu Gln Val Ala Leu Glu Glu Phe His Lys His Pro Pro Val Gln Trp	207
30 35 40 45	
gcc ttc cag gag acc agt gtg gag agc gcc gtg gac acg ccc ttc cca Ala Phe Gln Glu Thr Ser Val Glu Ser Ala Val Asp Thr Pro Phe Pro	255
50 55 60	
gct gga ata ttt gtg agg ctg gaa ttt aag ctg cag cag aca agc tgc Ala Gly Ile Phe Val Arg Leu Glu Phe Lys Leu Gln Gln Thr Ser Cys	303
65 70 75	
cgg aag agg gac tgg aag aaa ccc gag tgc aaa gtc agg ccc aat ggg Arg Lys Arg Asp Trp Lys Lys Pro Glu Cys Lys Val Arg Pro Asn Gly	351
80 85 90	
agg aaa cg ^g aaa tgc ctg gcc tgc atc aaa ctg ggc tct gag gac aaa Arg Lys Arg Lys Cys Leu Ala Cys Ile Lys Leu Gly Ser Glu Asp Lys	399
95 100 105	
gtt ctg ggc cgg ttg gtc cac tgc ccc ata gag acc caa gtt ctg cgg Val Leu Gly Arg Leu Val His Cys Pro Ile Glu Thr Gln Val Leu Arg	447
110 115 120 125	
gag gct gag gag cac cag gag acc cag tgc ctc agg gtg cag cgg gct Glu Ala Glu Glu His Gln Glu Thr Gln Cys Leu Arg Val Gln Arg Ala	495
130 135 140	
ggt gag gac ccc cac agc ttc tac ttc cct gga cag ttc gcc ttc tcc Gly Glu Asp Pro His Ser Phe Tyr Phe Pro Gly Gln Phe Ala Phe Ser	543
145 150 155	
aag gcc ctg ccc cgc agc taa gccagcactg agctgcgtgg tgcctccagg Lys Ala Leu Pro Arg Ser	594
160	
accgctgccc gtggtaacca gtggaagacc ccagcccca gggagaggac cccgttctat	654
ccccagccat gataataaag ctgctctccc agctgcctct c	695
<210> 13	
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<212> DNA	
<213> Homo sapiens	
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<222> (105)..(1436)	
<400> 13	
actgccttga aacgggctgg gcctgcctcg gacgccgccc gtgtcgccga ttctttcc	60
gcccgcctcca tggcggtgga tgcctgactg gaagcccgag tggg atg cgg ctg acg	116

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 Met Arg Leu Thr
 1

cgg aag cgg ctc tgc tcg ttt ctt atc gcc ctg tac tgc cta ttc tcc	164
Arg Lys Arg Leu Cys Ser Phe Leu Ile Ala Leu Tyr Cys Leu Phe Ser	
5 10 15 20	
ctc tac gct gcc tac cac gtc ttc ttc ggg cgc cgc cgc cag gcg ccg	212
Leu Tyr Ala Ala Tyr His Val Phe Phe Gly Arg Arg Arg Gln Ala Pro	
25 30 35	
gcc ggg tcc ccg cg ggc ctc agg aag ggg gcg gcc ccc gcg cgg gag	260
Ala Gly Ser Pro Arg Gly Leu Arg Lys Gly Ala Ala Pro Ala Arg Glu	
40 45 50	
aga cgc ggc cga gaa cag tcc act ttg gaa agt gaa gaa tgg aat cct	308
Arg Arg Gly Arg Glu Gln Ser Thr Leu Glu Ser Glu Glu Trp Asn Pro	
55 60 65	
tgg gaa gga gat gaa aaa aat gag caa caa cac aga ttt aaa act agc	356
Trp Glu Gly Asp Glu Lys Asn Glu Gln Gln His Arg Phe Lys Thr Ser	
70 75 80	
ctt caa ata tta gat aaa tcc acg aaa gga aaa aca gat ctc agt gta	404
Leu Gln Ile Leu Asp Lys Ser Thr Lys Gly Lys Thr Asp Leu Ser Val	
85 90 95 100	
caa atc tgg ggc aaa gct gcc att ggc ttg tat ctc tgg gag cat att	452
Gln Ile Trp Gly Lys Ala Ala Ile Gly Leu Tyr Leu Trp Glu His Ile	
105 110 115	
ttt gaa ggc tta ctt gat ccc agc gat gtg act gct caa tgg aga gaa	500
Phe Glu Gly Leu Leu Asp Pro Ser Asp Val Thr Ala Gln Trp Arg Glu	
120 125 130	
gga aag tca atc gta gga aga aca cag tac agc ttc atc act ggt cca	548
Gly Lys Ser Ile Val Gly Arg Thr Gln Tyr Ser Phe Ile Thr Gly Pro	
135 140 145	
gct gta ata cca ggg tac ttc tcc gtt gat gtg aat aat gtg gta ctc	596
Ala Val Ile Pro Gly Tyr Phe Ser Val Asp Val Asn Asn Val Val Leu	
150 155 160	
att tta aat gga aga gaa aaa gca aag atc ttt tat gcc acc cag tgg	644
Ile Leu Asn Gly Arg Glu Lys Ala Lys Ile Phe Tyr Ala Thr Gln Trp	
165 170 175 180	
tta ctt tat gca caa aat tta gtg caa att caa aaa ctc cag cat ctt	692
Leu Leu Tyr Ala Gln Asn Leu Val Gln Ile Gln Lys Leu Gln His Leu	
185 190 195	
gct gtt gtt ttg ctc gga aat gaa cat tgt gat aat gag tgg ata aac	740
Ala Val Val Leu Leu Gly Asn Glu His Cys Asp Asn Glu Trp Ile Asn	
200 205 210	
cca ttc ctc aaa aga aat gga ggc ttc gtg gag ctg ctt ttc ata ata	788
Pro Phe Leu Lys Arg Asn Gly Phe Val Glu Leu Leu Phe Ile Ile	
215 220 225	
tat gac agc ccc tgg att aat gac gtg gat gtt ttt cag tgg cct tta	836
Tyr Asp Ser Pro Trp Ile Asn Asp Val Asp Val Phe Gln Trp Pro Leu	
230 235 240	

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gga gta gca aca tac agg aat ttt cct gtg gtg gag gca agt tgg tca Gly Val Ala Thr Tyr Arg Asn Phe Pro Val Val Glu Ala Ser Trp Ser 245 250 255 260	884
atg ctg cat gat gag agg cca tat tta tgt aat ttc tta gga acg att Met Leu His Asp Glu Arg Pro Tyr Leu Cys Asn Phe Leu Gly Thr Ile 265 270 275	932
tat gaa aat tca tcc aga cag gca cta atg aac att ttg aaa aaa gat Tyr Glu Asn Ser Ser Arg Gln Ala Leu Met Asn Ile Leu Lys Lys Asp 280 285 290	980
ggg aac gat aag ctt tgt tgg gtt tca gca aga gaa cac tgg cag cct Gly Asn Asp Lys Leu Cys Trp Val Ser Ala Arg Glu His Trp Gln Pro 295 300 305	1028
cag gaa aca aat gaa agt ctt aag aat tac caa gat gcc ttg ctt cag Gln Glu Thr Asn Glu Ser Leu Lys Asn Tyr Gln Asp Ala Leu Leu Gln 310 315 320	1076
agt gat ctc aca ttg tgc ccg gtc gga gta aac aca gaa tgc tat cga Ser Asp Leu Thr Leu Cys Pro Val Gly Val Asn Thr Glu Cys Tyr Arg 325 330 335 340	1124
atc tat gag gct tgc tcc tat ggc tcc att cct gtg gtg gaa gac gtg Ile Tyr Glu Ala Cys Ser Tyr Gly Ser Ile Pro Val Val Glu Asp Val 345 350 355	1172
atg aca gct ggc aac tgt ggg aat aca tct gtg cac cac ggt gct cct Met Thr Ala Gly Asn Cys Gly Asn Thr Ser Val His His Gly Ala Pro 360 365 370	1220
ctg cag tta ctc aag tcc atg ggt gct ccc ttt atc ttt atc aag aac Leu Gln Leu Leu Lys Ser Met Gly Ala Pro Phe Ile Phe Ile Lys Asn 375 380 385	1268
tgg aag gaa ctc cct gct gtt tta gaa aaa gag aaa act ata att tta Trp Lys Glu Leu Pro Ala Val Leu Glu Lys Glu Lys Thr Ile Ile Leu 390 395 400	1316
caa gaa aaa att gaa aga aga aaa atg tta ctt cag tgg tat cag cac Gln Glu Lys Ile Glu Arg Arg Lys Met Leu Leu Gln Trp Tyr Gln His 405 410 415 420	1364
ttc aag aca gag ctt aaa atg aaa ttt act aat att tta gaa agc tca Phe Lys Thr Glu Leu Lys Met Lys Phe Thr Asn Ile Leu Glu Ser Ser 425 430 435	1412
ttt tta atg aat aat aaa agt taa ttatctttt gagct Phe Leu Met Asn Asn Lys Ser 440	1451

<210> 14
<211> 72
<212> PRT
<213> Artificial

<220>
<223> Synthetic Construct

<400> 14

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Met Ser Asp Ser Lys Glu Pro Arg Val Gln Gln Leu Gly Leu Leu Gly
1 5 10 15

Cys Leu Gly His Gly Ala Leu Val Leu Gln Leu Leu Ser Phe Met Leu
20 25 30

Leu Ala Gly Val Leu Val Ala Ile Leu Val Gln Val Ser Lys Val Pro
35 40 45

Ser Ser Leu Ser Gln Glu Gln Ser Glu Gln Asp Ala Ile Tyr Gln Asn
50 55 60

Leu Thr Gln Leu Lys Ala Ala Val
65 70

<210> 15
<211> 128
<212> PRT
<213> Artificial

<220>
<223> Synthetic Construct

<400> 15

Met Lys Tyr Leu Arg His Arg Arg Pro Asn Ala Thr Leu Ile Leu Ala
1 5 10 15

Ile Gly Ala Phe Thr Leu Leu Leu Phe Ser Leu Leu Val Ser Pro Pro
20 25 30

Thr Cys Lys Val Gln Glu Gln Pro Pro Ala Ile Pro Glu Ala Leu Ala
35 40 45

Trp Pro Thr Pro Pro Thr Arg Pro Ala Pro Ala Pro Cys His Ala Asn
50 55 60

Thr Ser Met Val Thr His Pro Asp Phe Ala Thr Gln Pro Gln His Val
65 70 75 80

Gln Asn Phe Leu Leu Tyr Arg His Cys Arg His Phe Pro Leu Leu Gln
85 90 95

Asp Val Pro Pro Ser Lys Cys Ala Gln Pro Val Phe Leu Leu Leu Val
100 105 110

Ile Lys Ser Ser Pro Ser Asn Tyr Val Arg Arg Glu Leu Leu Arg Arg
115 120 125

<210> 16

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<211> 50
<212> PRT
<213> Artificial

<220>
<223> Synthetic Construct

<400> 16

Met Lys Gly Trp Gly Trp Leu Ala Leu Leu Leu Gly Ala Leu Leu Gly
1 5 10 15

Thr Ala Trp Ala Arg Arg Ser Gln Asp Leu His Cys Gly Ala Cys Arg
20 25 30

Ala Leu Val Asp Glu Leu Glu Trp Glu Ile Ala Gln Val Asp Pro Lys
35 40 45

Lys Thr
50

<210> 17
<211> 135
<212> PRT
<213> Artificial

<220>
<223> Synthetic Construct

<400> 17

Met Arg Arg Leu Leu Ile Pro Leu Ala Leu Trp Leu Gly Ala Val Gly
1 5 10 15

Val Gly Val Ala Glu Leu Thr Glu Ala Gln Arg Arg Gly Leu Gln Val
20 25 30

Ala Leu Glu Glu Phe His Lys His Pro Pro Val Gln Trp Ala Phe Gln
35 40 45

Glu Thr Ser Val Glu Ser Ala Val Asp Thr Pro Phe Pro Ala Gly Ile
50 55 60

Phe Val Arg Leu Glu Phe Lys Leu Gln Gln Thr Ser Cys Arg Lys Arg
65 70 75 80

Asp Trp Lys Lys Pro Glu Cys Lys Val Arg Pro Asn Gly Arg Lys Arg
85 90 95

Lys Cys Leu Ala Cys Ile Lys Leu Gly Ser Glu Asp Lys Val Leu Gly
100 105 110

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Arg Leu Val His Cys Pro Ile Glu Thr Gln Val Leu Arg Glu Ala Glu
115 120 125

Glu His Gln Glu Thr Gln Cys
130 135

<210> 18
<211> 148
<212> PRT
<213> Artificial

<220>
<223> Synthetic Construct

<400> 18

Met Arg Leu Thr Arg Lys Arg Leu Cys Ser Phe Leu Ile Ala Leu Tyr
1 5 10 15

Cys Leu Phe Ser Leu Tyr Ala Ala Tyr His Val Phe Phe Gly Arg Arg
20 25 30

Arg Gln Ala Pro Ala Gly Ser Pro Arg Gly Leu Arg Lys Gly Ala Ala
35 40 45

Pro Ala Arg Glu Arg Arg Gly Arg Glu Gln Ser Thr Leu Glu Ser Glu
50 55 60

Glu Trp Asn Pro Trp Glu Gly Asp Glu Lys Asn Glu Gln Gln His Arg
65 70 75 80

Phe Lys Thr Ser Leu Gln Ile Leu Asp Lys Ser Thr Lys Gly Lys Thr
85 90 95

Asp Leu Ser Val Gln Ile Trp Gly Lys Ala Ala Ile Gly Leu Tyr Leu
100 105 110

Trp Glu His Ile Phe Glu Gly Leu Leu Asp Pro Ser Asp Val Thr Ala
115 120 125

Gln Trp Arg Glu Gly Lys Ser Ile Val Gly Arg Thr Gln Tyr Ser Phe
130 135 140

Ile Thr Gly Pro
145